What is claimed is:

1. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

a) a nucleic acid sequence encoding an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) a nucleic acid sequence encoding an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) a nucleic acid sequence encoding an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) a nucleic acid sequence encoding an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

e) a nucleic acid sequence encoding an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

f) a nucleic acid sequence that is fully complementary to the nucleic acid sequence of (a), (b), (c), (d), or (e).

2. The isolated nucleic acid molecule of Claim 1, wherein the nucleic sequence is selected from the group consisting of:

a) a nucleic acid sequence encoding an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

b) a nucleic acid sequence encoding an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

3. The isolated nucleic acid molecule of Claim 1, wherein the nucleic sequence is selected from the group consisting of: a nucleic acid sequence encoding an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

4. The isolated nucleic acid molecule of Claim 1, wherein the nucleic sequence is selected from the group consisting of: a nucleic acid sequence encoding an amino acid sequence that is at least about 90% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID

NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

5. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid sequence encodes an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and biologically active fragments thereof.

6. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid sequence is selected from the group consisting of: SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, and SEQ ID NO:67.

7. A recombinant nucleic acid molecule comprising the nucleic acid molecule of Claim 1, operatively linked to at least one transcription control sequence.

8. A recombinant cell transfected with the recombinant nucleic acid molecule of Claim 7.

9. A genetically modified microorganism, wherein the microorganism expresses a PKS system comprising at least one biologically active domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID

NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

wherein the microorganism is genetically modified to affect the activity of the PKS system.

10. The genetically modified microorganism of Claim 9, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

b) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

11. The genetically modified microorganism of Claim 9, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

12. The genetically modified microorganism of Claim 9, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence that is at least about 90% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

13. The genetically modified microorganism of Claim 9, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68 and biologically active fragments thereof.

14. The genetically modified microorganism of Claim 9, wherein the microorganism is genetically modified by transfection with a recombinant nucleic acid

molecule encoding the at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

15. The genetically modified microorganism of Claim 14, wherein the microorganism is a Thraustochytrid.

16. The genetically modified microorganism of Claim 14, wherein the microorganism is a *Schizochytrium*.

17. The genetically modified microorganism of Claim 14, wherein the microorganism has been further genetically modified to recombinantly express at least one nucleic acid molecule encoding at least one biologically active domain from a PKS system selected from the group consisting of: a bacterial PUFA PKS system, a Type I PKS system, a Type II PKS system, a modular PKS system, and a non-bacterial PUFA PKS system.

18. The genetically modified microoganism of Claim 17, wherein the non-bacterial PUFA PKS system is a Thraustochytrid PUFA PKS system.

19. The genetically modified microorganism of Claim 18, wherein the Thraustochytrid PUFA PKS system is a *Schizochytrium* PUFA PKS system.

20. The genetically modified microorganism of Claim 9, wherein the microorganism endogenously expresses a PKS system comprising the at least one domain of the PUFA PKS system, and wherein the genetic modification is in a nucleic acid sequence encoding at least one domain of the PUFA PKS system.

21. The genetically modified microorganism of Claim 20, wherein the microorganism has been further genetically modified to recombinantly express at least one nucleic acid molecule encoding at least one biologically active domain from a PKS system selected from the group consisting of: a bacterial PUFA PKS system, a Type I PKS system, a Type II PKS system, a modular PKS system, and a non-bacterial PUFA PKS system.

22. The genetically modified microorganism of Claim 21, wherein the non-bacterial PUFA PKS system is a Thraustochytrid PUFA PKS system.

23. The genetically modified microorganism of Claim 22, wherein the Thraustochytrid PUFA PKS system is a *Schizochytrium* PUFA PKS system.

24. The genetically modified microorganism of Claim 9, wherein the microorganism endogenously expresses a PUFA PKS system comprising the at least one biologically active domain of a PUFA PKS system, and wherein the genetic modification comprises expression of a recombinant nucleic acid molecule selected from the group consisting of a recombinant nucleic acid molecule encoding at least one biologically active domain from a second PKS system and a recombinant nucleic acid molecule encoding a protein that affects the activity of the endogenous PUFA PKS system.

25. The genetically modified microorganism of Claim 24, wherein the biologically active domain from a second PKS system is selected from the group consisting of:

a) a domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system from a Thraustochytrid microorganism;

b) a domain of a PUFA PKS system from a microorganism identified by the following method:

i) selecting a microorganism that produces at least one PUFA; and,

ii) identifying a microorganism from (i) that has an ability to produce increased PUFAs under dissolved oxygen conditions of less than about 5% of saturation in the fermentation medium, as compared to production of PUFAs by the microorganism under dissolved oxygen conditions of greater than about 5% of saturation in the fermentation medium;

c) a domain comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, and biologically active fragments thereof; and

d) a domain comprising an amino acid sequence that is at least about 60% identical to the amino acid sequence of (c), wherein the amino acid sequence

has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

26. The genetically modified microorganism of Claim 24, wherein the recombinant nucleic acid molecule encodes a phosphopantetheine transferase.

27. The genetically modified microorganism of Claim 24, wherein the second PKS system is selected from the group consisting of: a bacterial PUFA PKS system, a type I PKS system, a type II PKS system, a modular PKS system, and a non-bacterial PUFA PKS system.

28. The genetically modified microorganism of Claim 27, wherein the non-bacterial PUFA-PKS system is a eukaryotic PUFA PKS system.

29. The genetically modified microorganism of Claim 28, wherein the eukaryotic PUFA PKS system is a Thraustochytrid PUFA PKS system.

30. The genetically modified microorganism of Claim 29, wherein the Thraustochytrid PUFA PKS system is a *Schizochytrium* PUFA PKS system.

31. A genetically modified plant, wherein the plant has been genetically modified to recombinantly express a PKS system comprising at least one biologically active domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system, wherein the domain comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

32. The genetically modified plant of Claim 31, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

b) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

33. The genetically modified plant of Claim 31, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

34. The genetically modified plant of Claim 31, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence that is at least about 90% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

35. The genetically modified plant of Claim 31, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66 and SEQ ID NO:68 and biologically active fragments thereof.

36. The genetically modified plant of Claim 31, wherein the plant has been further genetically modified to recombinantly express at least one nucleic acid molecule encoding at least one biologically active domain from a PKS system selected from the group consisting of: a bacterial PUFA PKS system, a Type I PKS system, a Type II PKS system, a modular PKS system, and a non-bacterial PUFA PKS system.

37. The genetically modified plant of Claim 36, wherein the non-bacterial PUFA PKS system is a Thraustochytrid PUFA PKS system.

38. The genetically modified plant of Claim 37, wherein the Thraustochytrid PUFA PKS system is a *Schizochytrium* PUFA PKS system.

39. A method to produce a bioactive molecule that is produced by a polyketide synthase system, comprising culturing under conditions effective to produce the bioactive molecule a genetically modified organism that expresses a PKS system comprising at least one biologically active domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity

of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

40. The method of Claim 39, wherein the organism endogenously expresses a PKS system comprising the at least one domain of the PUFA PKS system, and wherein the genetic modification is in a nucleic acid sequence encoding the at least one domain of the PUFA PKS system.

41. The method of Claim 40, wherein the genetic modification changes at least one product produced by the endogenous PKS system, as compared to an organism wherein the PUFA PKS system has not been genetically modified.

42. The method of Claim 39, wherein the organism endogenously expresses a PKS system comprising the at least one biologically active domain of the PUFA PKS system, and wherein the genetic modification comprises transfection of the organism with a recombinant nucleic acid molecule selected from the group consisting of: a recombinant nucleic acid molecule encoding at least one biologically active domain from a second PKS system and a recombinant nucleic acid molecule encoding a protein that affects the activity of the PUFA PKS system.

43. The method of Claim 42, wherein the genetic modification changes at least one product produced by the endogenous PKS system, as compared to an organism that has not been genetically modified to affect PUFA production.

44. The method of Claim 39, wherein the organism is genetically modified by transfection with a recombinant nucleic acid molecule encoding the at least one domain of the polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

45. The method of Claim 39, wherein the organism produces a polyunsaturated fatty acid (PUFA) profile that differs from the naturally occurring organism without a genetic modification.

46. The method of Claim 39, wherein the organism endogenously expresses a non-bacterial PUFA PKS system, and wherein the genetic modification comprises substitution of a domain from a different PKS system for a nucleic acid sequence encoding at least one domain of the non-bacterial PUFA PKS system.

47. The method of Claim 39, wherein the organism endogenously expresses a non-bacterial PUFA PKS system that has been modified by transfecting the organism with a recombinant nucleic acid molecule encoding a protein that regulates the chain length of fatty acids produced by the PUFA PKS system.

48. The method of Claim 39, wherein the bioactive molecule is selected from the group consisting of: an anti-inflammatory formulation, a chemotherapeutic agent, an active excipient, an osteoporosis drug, an anti-depressant, an anti-convulsant, an anti-*Heliobactor pylori* drug, a drug for treatment of neurodegenerative disease, a drug for treatment of degenerative liver disease, an antibiotic, and a cholesterol lowering formulation.

49. The method of Claim 39, wherein the bioactive molecule is an antibiotic.

50. The method of Claim 39, wherein the bioactive molecule is a polyunsaturated fatty acid (PUFA).

51. The method of Claim 39, wherein the bioactive molecule is a molecule including carbon-carbon double bonds in the *cis* configuration.

52. The method of Claim 39, wherein the bioactive molecule is a molecule including a double bond at every third carbon.

53. The method of Claim 39, wherein the organism is a microorganism.

54. The method of Claim 39, wherein the organism is a plant.

55. A method to produce a plant that has a polyunsaturated fatty acid (PUFA) profile that differs from the naturally occurring plant, comprising genetically modifying cells of the plant to express a PKS system comprising at least one recombinant nucleic acid molecule comprising a nucleic acid sequence encoding at least one biologically active domain of a PUFA PKS system, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

56. A method to modify an endproduct containing at least one fatty acid, comprising adding to the endproduct an oil produced by a recombinant host cell that expresses at least one recombinant nucleic acid molecule comprising a nucleic acid sequence encoding at least one biologically active domain of a PUFA PKS system, wherein the at least one domain of a PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

57. The method of Claim 56, wherein the endproduct is selected from the group consisting of a dietary supplement, a food product, a pharmaceutical formulation, a humanized animal milk, and an infant formula.

58. The method of Claim 57, wherein the pharmaceutical formulation is selected from the group consisting of an anti-inflammatory formulation, a chemotherapeutic agent, an active excipient, an osteoporosis drug, an anti-depressant, an anti-convulsant, an anti-*Heliobactor pylori* drug, a drug for treatment of neurodegenerative disease, a drug for treatment of degenerative liver disease, an antibiotic, and a cholesterol lowering formulation.

59. The method of Claim 56, wherein the endproduct is used to treat a condition selected from the group consisting of: chronic inflammation, acute inflammation, gastrointestinal disorder, cancer, cachexia, cardiac restenosis, neurodegenerative disorder,

degenerative disorder of the liver, blood lipid disorder, osteoporosis, osteoarthritis, autoimmune disease, preeclampsia, preterm birth, age related maculopathy, pulmonary disorder, and peroxisomal disorder.

60. A method to produce a humanized animal milk, comprising genetically modifying milk-producing cells of a milk-producing animal with at least one recombinant nucleic acid molecule comprising a nucleic acid sequence encoding at least one biologically active domain of a PUFA PKS system, wherein the at least one domain of the PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof;

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:39, SEQ ID NO:43, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:56 and SEQ ID NO:58, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

c) an amino acid sequence that is at least about 65% identical to SEQ ID NO:54, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system;

d) an amino acid sequence that is at least about 70% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:62 and SEQ ID NO:64, wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system; and

e) an amino acid sequence that is at least about 80% identical to an amino acid sequence selected from the group consisting of: SEQ ID NO:41, SEQ ID NO:66, SEQ ID NO:68, wherein the amino acid sequence has a biological activity

of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

61. A genetically modified Thraustochytrid microorganism, wherein the microorganism has an endogenous polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system, and wherein the endogenous PUFA PKS system has been genetically modified to alter the expression profile of a polyunsaturated fatty acid (PUFA) by the Thraustochytrid microorganism as compared to the Thraustochytrid microorganism in the absence of the genetic modification.

62. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the endogenous PUFA PKS system has been modified by mutagenesis of a nucleic acid sequence that encodes at least one domain of the endogenous PUFA PKS system.

63. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the endogenous PUFA PKS system has been modified by deleting at least one nucleic acid sequence that encodes at least one domain of the endogenous PUFA PKS system and inserting therefore a nucleic acid sequence encoding a homologue of the endogenous domain to alter the PUFA production profile of the Thraustochytrid microorganism, wherein the homologue has a biological activity of at least one domain of a PKS system.

64. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the endogenous PUFA PKS system has been modified by deleting at least one nucleic acid sequence that encodes at least one domain of the endogenous PUFA PKS system and inserting therefore a nucleic acid sequence encoding at least one domain of a PKS system from a different microorganism.

65. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system is a domain having a biological activity of at least one of the following proteins: malonyl-CoA:ACP acyltransferase (MAT), β-keto acyl-ACP synthase (KS), ketoreductase (KR), acyltransferase (AT), FabA-like β-hydroxy acyl-ACP dehydrase (DH), phosphopantetheine transferase, chain length factor (CLF), acyl carrier protein (ACP), enoyl ACP-reductase (ER), an enzyme that catalyzes the synthesis of *trans*-2-acyl-ACP, an enzyme that catalyzes the reversible

isomerization of *trans*-2-acyl-ACP to *cis*-3-acyl-ACP, and an enzyme that catalyzes the elongation of *cis*-3-acyl-ACP to *cis*-5-β-keto-acyl-ACP.

66. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system comprises an amino acid sequence selected from the group consisting of:

a) an amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68 and biologically active fragments thereof; and

b) an amino acid sequence that is at least about 60% identical to an amino acid sequence of (a), wherein the amino acid sequence has a biological activity of at least one domain of a polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system.

67. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system comprises an amino acid sequence that is at least about 70% identical to the amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68.

68. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system comprises an amino acid sequence that is at least about 80% identical to the amino acid sequence selected

from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68.

69. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system comprises an amino acid sequence that is at least about 90% identical to the amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68.

70. The genetically modified Thraustochytrid microorganism of any one of Claims 62-64, wherein the domain of the endogenous PUFA PKS system comprises an amino acid sequence selected from the group consisting of: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:13, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, and biologically active fragments thereof.

71. The genetically modified Thraustochytrid microorganism of Claim 62, wherein the modification is produced by targeted mutagenesis.

72. The genetically modified Thraustochytrid microorganism of Claim 62, wherein the modification is produced by classical mutagenesis and screening.

73. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the homologue of the endogenous domain comprises a modification, as compared to the endogenous domain, selected from the group consisting of at least one deletion, insertion or substitution that results in an alteration of PUFA production profile by the microorganism.

74. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the amino acid sequence of the homologue is at least about 60% identical to the amino acid sequence of the endogenous domain.

75. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the amino acid sequence of the homologue is at least about 70% identical to the amino acid sequence of the endogenous domain.

76. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the amino acid sequence of the homologue is at least about 80% identical to the amino acid sequence of the endogenous domain.

77. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the amino acid sequence of the homologue is at least about 90% identical to the amino acid sequence of the endogenous domain.

78. The genetically modified Thraustochytrid microorganism of Claim 63, wherein the homologue of the endogenous domain is a domain from a PUFA PKS system of another Thraustochytrid microorganism.

79. The genetically modified Thraustochytrid microorganism of Claim 64, wherein the nucleic acid sequence encoding at least one domain of a PKS system from a different microorganism is from a bacterial PUFA PKS system.

80. The genetically modified Thraustochytrid microorganism of Claim 79, wherein the different microorganism is a marine bacteria having a PUFA PKS system that naturally produces PUFAs at a temperature of about 25°C or greater.

81. The genetically modified Thraustochytrid microorganism of Claim 80, wherein the marine bacteria is selected from the group consisting of *Shewanella olleyana* and *Shewanella japonica*.

82. The genetically modified Thraustochytrid microorganism of Claim 64, wherein the domain of a PKS system from a different microorganism is from a PKS system selected from the group consisting of: a Type I PKS system, a Type II PKS system, a modular PKS system, and a PUFA PKS system from a different Thraustochytrid microorganism.

83. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the PUFA production profile is altered to initiate, increase or decrease production of eicosapentaenoic acid (EPA) by the microorganism.

84. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the PUFA production profile is altered to initiate, increase or decrease production of docosahexaenoic acid (DHA) by the microorganism.

85. The genetically modified Thraustochytrid microorganism of Claim 61; wherein the PUFA production profile is altered to initiate, increase or decrease production of one or both isomers of docosapentaenoic acid (DPA) by the microorganism.

86. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the PUFA production profile is altered to initiate, increase or decrease production of arachidonic acid (ARA) by the microorganism.

87. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the Thraustochytrid is from a genus selected from the group consisting of *Schizochytrium, Thraustochytrium*, and *Japonochytrium*.

88. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the Thraustochytrid is from the genus *Schizochytrium*.

89. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the Thraustochytrid is from a *Schizochytrium* species selected from the group consisting of: *Schizochytrium aggregatum*, *Schizochytrium limacinum*, and *Schizochytrium minutum*.

90. The genetically modified Thraustochytrid microorganism of Claim 61, wherein the Thraustochytrid is from the genus *Thraustochytrium*.

91. A genetically modified *Schizochytrium* that produces eicosapentaenoic acid (EPA), wherein the *Schizochytrium* has an endogenous polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system comprising a genetic modification in at least one nucleic acid sequence that encodes at least one domain of the endogenous PUFA PKS system that results in the production of EPA by the *Schizochytrium*.

92. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding at least one domain having a biological activity of at least one of the following proteins: malonyl-CoA:ACP acyltransferase (MAT), β-keto acyl-ACP synthase (KS), ketoreductase (KR), acyltransferase (AT), FabA-like β-hydroxy acyl-ACP dehydrase (DH), phosphopantetheine transferase, chain length factor (CLF), acyl carrier protein (ACP), enoyl ACP-reductase (ER), an enzyme that catalyzes the synthesis of *trans*-2-acyl-ACP, an enzyme that catalyzes the reversible isomerization of *trans*-2-acyl-ACP to *cis*-3-acyl-ACP, and an enzyme that catalyzes the elongation of *cis*-3-acyl-ACP to *cis*-5-β-keto-acyl-ACP.

93. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding at least one domain from the open reading frame encoding SEQ ID NO:2 of the endogenous PUFA PKS system.

94. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding at least one domain from the open reading frame encoding SEQ ID NO:4 of the endogenous PUFA PKS system.

95. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding at least one domain from the open reading frame encoding SEQ ID NO:6 of the endogenous PUFA PKS system.

96. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding at least one domain having a biological activity of at least one of the following

proteins: β-keto acyl-ACP synthase (KS), FabA-like β-hydroxy acyl-ACP dehydrase (DH), chain length factor (CLF), an enzyme that catalyzes the synthesis of *trans*-2-acyl-ACP, an enzyme that catalyzes the reversible isomerization of *trans*-2-acyl-ACP to *cis*-3-acyl-ACP, and an enzyme that catalyzes the elongation of *cis*-3-acyl-ACP to *cis*-5-β-keto-acyl-ACP.

97. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* comprises a genetic modification in at least one nucleic acid sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:28 and SEQ ID NO:30 of the endogenous PUFA PKS system.

98. The genetically modified *Schizochytrium* of Claim 91, wherein the *Schizochytrium* has been modified by deleting at least one nucleic acid sequence that encodes at least one domain of the endogenous PUFA PKS system and inserting therefore a nucleic acid sequence encoding at least one domain of a PKS system from a non-*Schizochytrium* microorganism.

99. The genetically modified *Schizochytrium* of Claim 98, wherein the non-*Schizochytrium* microorganism grows and produces PUFAs at temperature of at least about 15°C.

100. The genetically modified *Schizochytrium* of Claim 98, wherein the non-*Schizochytrium* microorganism grows and produces PUFAs at temperature of at least about 20°C.

101. The genetically modified *Schizochytrium* of Claim 98, wherein the non-*Schizochytrium* microorganism grows and produces PUFAs at temperature of at least about 25°C.

102. The genetically modified *Schizochytrium* of Claim 98, wherein the non-*Schizochytrium* microorganism grows and produces PUFAs at temperature of at least about 30°C.

103. The genetically modified *Schizochytrium* of Claim 98, wherein the non-*Schizochytrium* microorganism grows and produces PUFAs at temperature of between about 20°C and about 40°C.

104. The genetically modified *Schizochytrium* of Claim 98, wherein the nucleic acid sequence encoding at least one domain of a PKS system from a non-*Schizochytrium* microorganism is from a bacterial PUFA PKS system.

105. The genetically modified *Schizochytrium* of Claim 104, wherein the bacterial PUFA PKS system is from a bacterium selected from the group consisting of *Shewanella olleyana* and *Shewanella japonica*.

106. The genetically modified *Schizochytrium* of Claim 98, wherein the nucleic acid sequence encoding at least one domain of a PKS system is selected from the group consisting of a Type I PKS system, a Type II PKS system, a modular PKS system, and a non-bacterial PUFA PKS system.

107. The genetically modified *Schizochytrium* of Claim 106, wherein the non-bacterial PUFA-PKS system is a eukaryotic PUFA PKS system.

108. The genetically modified *Schizochytrium* of Claim 107, wherein the eukaryotic PUFA PKS system is a Thraustochytrid PUFA PKS system.

109. A genetically modified *Schizochytrium* that produces increased amounts of docosahexaenoic acid (DHA) as compared to a non-genetically modified *Schizochytrium*, wherein the *Schizochytrium* has an endogenous polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system comprising a genetic modification in at least one nucleic sequence that encodes at least one domain of the endogenous PUFA PKS system that results in increased the production of DHA by the *Schizochytrium*.

110. The genetically modified *Schizochytrium* of Claim 109, wherein at least one domain of the endogenous PUFA PKS system has been modified by substitution for at least one domain of a PUFA PKS system from *Thraustochytrium*.

111. The genetically modified *Schizochytrium* of Claim 109, wherein the ratio of DHA to DPA produced by the *Schizochytrium* is increased as compared to a non-genetically modified *Schizochytrium*.

112. A method to produce lipids enriched for at least one selected polyunsaturated fatty acid (PUFA), comprising culturing under conditions effective to produce the lipids a

genetically modified Thraustochytrid microorganism of Claim 61 or a genetically modified *Schizochytrium* according to Claim 91 or Claim 109.

113. The method of Claim 112, wherein the selected PUFA is eicosapentaenoic acid (EPA).

114. A method to produce eicosapentaenoic acid (EPA)-enriched lipids, comprising culturing under conditions effective to produce the EPA-enriched lipids a genetically modified Thraustochytrid microorganism, wherein the microorganism has an endogenous polyunsaturated fatty acid (PUFA) polyketide synthase (PKS) system, and wherein the endogenous PUFA PKS system has been genetically modified in at least one domain to initiate or increase the production of EPA in the lipids of the microorganism as compared to in the absence of the modification.